



SEQUENCE LISTING

<110> Callen, Walter
Richardson, Toby
Frey, Gerhard
Miller, Carl
Kazaoka, Martin
Short, Jay
Mathur, Eric

<120> ENZYMES HAVING ALPHA AMYLASE ACTIVITY
AND METHODS OF USE THEREOF

<130> 09010-107001

<140> 10/081,739

<141> 2002-02-21

<150> 60/270,495

<151> 2001-02-21

<150> 60/270,496

<151> 2001-02-21

<150> 60/291,122

<151> 2001-05-14

<160> 69

<170> FastSEQ for Windows Version 4.0

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<211> 1311

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetically generated

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gagacgcgct	ttggctccaa	gcaggagctc	gtgaacatga	taaacaccgc	ccacgcctat	300
ggcatgaagg	taatagccga	tatagtcatc	aaccaccgcg	ccggcggtga	cctggagtgg	360
aacccttcg	tgaacgacta	tacctggacc	gacttctcaa	aggtcgcgtc	gggtaaatac	420
acggccaact	acctcgactt	ccaccggaac	gagctccatg	cgggcgattc	cggaacattt	480
ggaggctatc	ccgacatatg	ccacgacaag	agctgggacc	agtactggct	ctggggccagc	540
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aaqccqtaaa	cctttqtaqc	aaaccacqac	accgatataa	tctggaacaa	qtatccaqcc	900
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tggtcaaca aggataagct caagaacctc atctggatac atgagaacct cgccggagga 1020
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tatgtgccga agttcgcggg cgcgtgcata cactagata ctggtaacct cggaggctgg 1200
gtagacaagt acgtctactc aagcggctgg gtctatctcg aagctccagc ttacgacct 1260
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<210> 2

<211> 436

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetically engineered

<400> 2

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Gln Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile Trp Ile
35          40          45
Pro Pro Ala Ser Lys Gly Met Gly Gly Ala Tyr Ser Met Gly Tyr Asp
50          55          60
Pro Tyr Asp Phe Phe Asp Leu Gly Glu Tyr Asp Gln Lys Gly Thr Val
65          70          75          80
Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Val Asn Met Ile Asn Thr
85          90          95
Ala His Ala Tyr Gly Met Lys Val Ile Ala Asp Ile Val Ile Asn His
100         105         110
Arg Ala Gly Asp Leu Glu Trp Asn Pro Phe Val Asn Asp Tyr Thr
115         120         125
Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr
130         135         140
Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly Thr Phe
145         150         155         160
Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln Tyr Trp
165         170         175
Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly
180         185         190
Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Ala Pro Trp Val
195         200         205
Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr
210         215         220
Trp Asp Thr Asn Val Asp Ala Val Leu Asn Trp Ala Tyr Ser Ser Gly
225         230         235         240
Ala Lys Val Phe Asp Phe Ala Leu Tyr Tyr Lys Met Asp Glu Ala Phe
245         250         255
Asp Asn Lys Asn Ile Pro Ala Leu Val Ser Ala Leu Gln Asn Gly Gln
260         265         270
Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn
275         280         285
His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile
290         295         300
Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu
305         310         315         320
Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His Glu Asn

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	325		330		335
Leu Ala Gly Gly Ser Thr Asp Ile Val Tyr Tyr Asp Asn Asp Glu Leu					
	340		345		350
Ile Phe Val Arg Asn Gly Tyr Gly Asp Lys Pro Gly Leu Ile Thr Tyr					
	355		360		365
Ile Asn Leu Gly Ser Ser Lys Ala Gly Arg Trp Val Tyr Val Pro Lys					
	370		375		380
Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp					
385		390		395	400
Val Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro					
	405		410		415
Ala Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr					
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Cys Gly Val Gly					
	435				

<210> 3

<211> 1419

<212> DNA

<213> Environmental

<400> 3

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gatggcacgt	tatggacca	agtggccaat	gaagccaaca	acttatccag	ccttggcatc	180
accgctcttt	ggctgccgcc	cgcttacaaa	ggaacaagcc	gcagcgacgt	agggtagcga	240
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ggaacaaaag	ctcaatatct	tcaagccatt	caagccgccc	acgccgctgg	aatgcaagtg	360
tacgccgatg	tcggtgttga	ccataaaggc	ggcgctgacg	gcacggaatg	ggtggacgcc	420
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tggacgaaat	ttgattttcc	cgggcggggc	aacacctact	ccagctttta	gtggcgctgg	540
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cgcggcatcg	gcaaagcgtg	ggattgggaa	gtagacacgg	aaaacggaaa	ctatgactac	660
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ctattttaccg	tcggggaata	ttggagctat	gacatcaaca	agttgcacaa	ttacattacg	900
aaaacagacg	gaacgatgtc	tttgtttgat	gccccgttac	acaacaaatt	ttataccgct	960
tccaaatcag	ggggcgcat	tgatatgcgc	acgttaatga	ccaatactct	catgaaagat	1020
caaccgacat	tggccgtcac	cttcgttgat	aatcatgaca	ccgaaccg	ccaagcgctg	1080
cagtcatggg	tcgacccatg	gttcaaaccg	ttggcttacg	cctttattct	aactcggcag	1140
gaaggatacc	cgtgcgtctt	ttatggtgac	tattatggca	ttccacaata	taacattcct	1200
tcgctgaaaa	gcaaaatcga	tccgctcctc	atcgcgcgca	gggattatgc	ttacggaacg	1260
caacatgatt	atcttgatca	ctccgacatc	atcgggtgga	caaggggaag	ggtcactgaa	1320
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<210> 4

<211> 1539

<212> DNA

<213> Environmental

<400> 4

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gcggatgtgg	gctacgggtgc	ttacgacctt	tatgatttag	gggagtttca	tcaaaaaggg	300
acggttcggg	caaagtacgg	cacaaaagga	gagctgcaat	ctgcatcaa	aagtcttcat	360
tcccgcgaca	ttaacgttta	cggggatgtg	gtcatcaacc	acaaaggcgg	cgctgatgcy	420
accgaagatg	taaccgcggt	tgaagtcgat	cccgtgacc	gcaaccgcgt	aatttcagga	480
gaacaccgaa	ttaaagcctg	gacacatttt	cattttccgg	ggcgcgcgag	cacatacagc	540
gattttaaat	ggcattggta	ccattttgac	ggaaccgatt	gggacgagtc	ccgaaagctg	600
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cccgggtgggg	caaagcgaat	gtatgtcggc	cggcaaaacg	ccgggtgagac	atggcatgac	1440
attaccggaa	accgttcgga	gccggttgct	atcaattcgg	aaggctgggg	agagtttcac	1500
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<210> 5

<211> 1395

<212> DNA

<213> Environmental

<400> 5

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aaaatcccgg	agtggtaaga	cgtcggaatc	tcggcgatat	ggattcctcc	agctagcaaa	240
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tactatcaga	agggaaacagt	tgagacgcgc	ttcggctcaa	aggaggaact	ggtgaacatg	360
ataaacaccg	cacactccta	tggcataaag	gtgatagcgg	acatagtcac	aaaccaccgc	420
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aaggctgcct	ccggtaaata	cacggccaac	taccttgact	tccacccaaa	cgaggtcaag	540
tgctgcgatg	agggtaacat	tggtgacttt	ccggacatcg	cccacgagaa	gagctgggat	600
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<210> 6

<211> 1386

<212> DNA

<213> Bacteria

<400> 6

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gccttctact gggacgtccc aggtggagga atctgggtggg acaccatcag gagcaagata      180
ccggagtggg acgagggcggg aatatccgcc atttggattc cgccagccag caaggggatg      240
agcggcgggt actcgatggg ctacgatccc tacgatttct ttgacctcgg cgagtacaac      300
cagaagggaa ccatcgaaac gcgctttggc tctaaacagg agctcatcaa tatgataaac      360
acggcccatg cctacggcat aaaggtcata gcggacatcg tcataaacca ccgcgaggc      420
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aacctcggag gctgggtaga caagtacgtc tactcaagcg gctgggtcta tctcgaagct     1320
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<210> 7

<211> 472

<212> PRT

<213> Environmental

<400> 7

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             20             25             30
Tyr Phe Glu Trp Tyr Leu Pro Asp Asp Gly Thr Leu Trp Thr Lys Val
             35             40             45
Ala Asn Glu Ala Asn Asn Leu Ser Ser Leu Gly Ile Thr Ala Leu Trp
             50             55             60
Leu Pro Pro Ala Tyr Lys Gly Thr Ser Arg Ser Asp Val Gly Tyr Gly
65             70             75             80
Val Tyr Asp Leu Tyr Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val
             85             90             95
Arg Thr Lys Tyr Gly Thr Lys Ala Gln Tyr Leu Gln Ala Ile Gln Ala
             100            105            110
Ala His Ala Ala Gly Met Gln Val Tyr Ala Asp Val Val Phe Asp His
             115            120            125
Lys Gly Gly Ala Asp Gly Thr Glu Trp Val Asp Ala Val Glu Val Asn
             130            135            140
Pro Ser Asp Arg Asn Gln Glu Ile Ser Gly Thr Tyr Gln Ile Gln Ala
145            150            155            160
Trp Thr Lys Phe Asp Phe Pro Gly Arg Gly Asn Thr Tyr Ser Ser Phe
             165            170            175
Lys Trp Arg Trp Tyr His Phe Asp Gly Val Asp Trp Asp Glu Ser Arg

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100					105					110					
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130					135					140					
Thr	Ala	Val	Glu	Val	Asp	Pro	Ala	Asp	Arg	Asn	Arg	Val	Ile	Ser	Gly
145					150					155					
Glu	His	Arg	Ile	Lys	Ala	Trp	Thr	His	Phe	His	Phe	Pro	Gly	Arg	Gly
165					170					175					
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210					215					220					
Leu	Met	Tyr	Ala	Asp	Ile	Asp	Tyr	Asp	His	Pro	Asp	Val	Ala	Ala	Glu
225					230					235					
Ile	Lys	Arg	Trp	Gly	Thr	Trp	Tyr	Ala	Asn	Glu	Leu	Gln	Leu	Asp	Gly
245					250					255					
Phe	Arg	Leu	Asp	Ala	Val	Lys	His	Ile	Lys	Phe	Ser	Phe	Leu	Arg	Asp
260					265					270					
Trp	Val	Asn	His	Val	Arg	Glu	Lys	Thr	Gly	Lys	Glu	Met	Phe	Thr	Val
275					280					285					
Ala	Glu	Tyr	Trp	Gln	Asn	Asp	Leu	Gly	Ala	Leu	Glu	Asn	Tyr	Leu	Asn
290					295					300					
Lys	Thr	Asn	Phe	Asn	His	Ser	Val	Phe	Asp	Val	Pro	Leu	His	Tyr	Gln
305					310					315					
Phe	His	Ala	Ala	Ser	Thr	Gln	Gly	Gly	Gly	Tyr	Asp	Met	Arg	Lys	Leu
325					330					335					
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340					345					350					
Val	Asp	Asn	His	Asp	Thr	Gln	Pro	Gly	Gln	Ser	Leu	Glu	Ser	Thr	Val
355					360					365					
Gln	Thr	Trp	Phe	Lys	Pro	Leu	Ala	Tyr	Ala	Phe	Ile	Leu	Thr	Arg	Glu
370					375					380					
Ser	Gly	Tyr	Pro	Gln	Val	Phe	Tyr	Gly	Asp	Met	Tyr	Gly	Thr	Lys	Gly
385					390					395					
Asp	Ser	Gln	Arg	Glu	Ile	Pro	Ala	Leu	Lys	His	Lys	Ile	Glu	Pro	Ile
405					410					415					
Leu	Lys	Ala	Arg	Lys	Gln	Tyr	Ala	Tyr	Gly	Ala	Gln	His	Asp	Tyr	Phe
420					425					430					
Asp	His	His	Asp	Ile	Val	Gly	Trp	Thr	Arg	Glu	Gly	Asp	Ser	Ser	Val
435					440					445					
Ala	Asn	Ser	Gly	Leu	Ala	Ala	Leu	Ile	Thr	Asp	Gly	Pro	Gly	Gly	Ala
450					455					460					
Lys	Arg	Met	Tyr	Val	Gly	Arg	Gln	Asn	Ala	Gly	Glu	Thr	Trp	His	Asp
465					470					475					
Ile	Thr	Gly	Asn	Arg	Ser	Glu	Pro	Val	Val	Ile	Asn	Ser	Glu	Gly	Trp
485					490					495					
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500					505					510					

<210> 9

<211> 464

<212> PRT

<213> Environmental

<400> 9

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			20					25					30		
Glu	Leu	Glu	Glu	Gly	Gly	Val	Ile	Met	Gln	Ala	Phe	Tyr	Trp	Asp	Val
		35					40					45			
Pro	Gly	Gly	Gly	Ile	Trp	Trp	Asp	Thr	Ile	Arg	Gln	Lys	Ile	Pro	Glu
	50					55					60				
Trp	Tyr	Asp	Ala	Gly	Ile	Ser	Ala	Ile	Trp	Ile	Pro	Pro	Ala	Ser	Lys
65					70					75					80
Gly	Met	Gly	Gly	Gly	Tyr	Ser	Met	Gly	Tyr	Asp	Pro	Tyr	Asp	Phe	Phe
				85					90					95	
Asp	Leu	Gly	Glu	Tyr	Tyr	Gln	Lys	Gly	Thr	Val	Glu	Thr	Arg	Phe	Gly
			100					105					110		
Ser	Lys	Glu	Glu	Leu	Val	Asn	Met	Ile	Asn	Thr	Ala	His	Ser	Tyr	Gly
		115					120					125			
Ile	Lys	Val	Ile	Ala	Asp	Ile	Val	Ile	Asn	His	Arg	Ala	Gly	Gly	Asp
	130					135					140				
Leu	Glu	Trp	Asn	Pro	Phe	Val	Asn	Asn	Tyr	Thr	Trp	Thr	Asp	Phe	Ser
145					150					155					160
Lys	Val	Ala	Ser	Gly	Lys	Tyr	Thr	Ala	Asn	Tyr	Leu	Asp	Phe	His	Pro
				165					170					175	
Asn	Glu	Val	Lys	Cys	Cys	Asp	Glu	Gly	Thr	Phe	Gly	Asp	Phe	Pro	Asp
			180					185					190		
Ile	Ala	His	Glu	Lys	Ser	Trp	Asp	Gln	Tyr	Trp	Leu	Trp	Ala	Ser	Asn
	195					200						205			
Glu	Ser	Tyr	Ala	Ala	Tyr	Leu	Arg	Ser	Ile	Gly	Ile	Asp	Ala	Trp	Arg
	210					215					220				
Phe	Asp	Tyr	Val	Lys	Gly	Tyr	Gly	Ala	Trp	Val	Val	Asn	Asp	Trp	Leu
225				230						235					240
Ser	Trp	Trp	Gly	Gly	Trp	Ala	Val	Gly	Glu	Tyr	Trp	Asp	Thr	Asn	Val
			245						250					255	
Asp	Ala	Leu	Leu	Asn	Trp	Ala	Tyr	Asp	Ser	Gly	Ala	Lys	Val	Phe	Asp
		260						265					270		
Phe	Pro	Leu	Tyr	Tyr	Lys	Met	Asp	Glu	Ala	Phe	Asp	Asn	Thr	Asn	Ile
	275						280					285			
Pro	Ala	Leu	Val	Tyr	Ala	Leu	Gln	Asn	Gly	Gly	Thr	Val	Val	Ser	Arg
	290					295					300				
Asp	Pro	Phe	Lys	Ala	Val	Thr	Phe	Val	Ala	Asn	His	Asp	Thr	Asp	Ile
305					310					315					320
Ile	Trp	Asn	Lys	Tyr	Pro	Ala	Tyr	Ala	Phe	Ile	Leu	Thr	Tyr	Glu	Gly
			325						330					335	
Gln	Pro	Val	Ile	Phe	Tyr	Arg	Asp	Tyr	Glu	Glu	Trp	Leu	Asn	Lys	Asp
		340						345					350		
Lys	Leu	Asn	Asn	Leu	Ile	Trp	Ile	His	Glu	His	Leu	Ala	Gly	Gly	Ser
	355						360					365			
Thr	Lys	Ile	Leu	Tyr	Tyr	Asp	Asn	Asp	Glu	Leu	Ile	Phe	Met	Arg	Glu
	370					375					380				
Gly	Tyr	Gly	Ser	Lys	Pro	Gly	Leu	Ile	Thr	Tyr	Ile	Asn	Leu	Gly	Asn
385				390						395					400
Asp	Trp	Ala	Glu	Arg	Trp	Val	Asn	Val	Gly	Ser	Lys	Phe	Ala	Gly	Tyr
			405						410					415	
Thr	Ile	His	Glu	Tyr	Thr	Gly	Asn	Leu	Gly	Gly	Trp	Val	Asp	Arg	Trp
			420					425					430		
Val	Gln	Tyr	Asp	Gly	Trp	Val	Lys	Leu	Thr	Ala	Pro	Pro	His	Asp	Pro
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<211> 461

<212> PRT

<213> Bacteria

<400> 10

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 1 5 10 15
 Met Ala Val Val Ala Gln Pro Ala Ser Ala Ala Lys Tyr Ser Glu Leu
 20 25 30
 Glu Glu Gly Gly Val Ile Met Gln Ala Phe Tyr Trp Asp Val Pro Gly
 35 40 45
 Gly Gly Ile Trp Trp Asp Thr Ile Arg Ser Lys Ile Pro Glu Trp Tyr
 50 55 60
 Glu Ala Gly Ile Ser Ala Ile Trp Ile Pro Pro Ala Ser Lys Gly Met
 65 70 75 80
 Ser Gly Gly Tyr Ser Met Gly Tyr Asp Pro Tyr Asp Phe Phe Asp Leu
 85 90 95
 Gly Glu Tyr Asn Gln Lys Gly Thr Ile Glu Thr Arg Phe Gly Ser Lys
 100 105 110
 Gln Glu Leu Ile Asn Met Ile Asn Thr Ala His Ala Tyr Gly Ile Lys
 115 120 125
 Val Ile Ala Asp Ile Val Ile Asn His Arg Ala Gly Gly Asp Leu Glu
 130 135 140
 Trp Asn Pro Phe Val Gly Asp Tyr Thr Trp Thr Asp Phe Ser Lys Val
 145 150 155 160
 Ala Ser Gly Lys Tyr Thr Ala Asn Tyr Leu Asp Phe His Pro Asn Glu
 165 170 175
 Val Lys Cys Cys Asp Glu Gly Thr Phe Gly Gly Phe Pro Asp Ile Ala
 180 185 190
 His Glu Lys Ser Trp Asp Gln His Trp Leu Trp Ala Ser Asp Glu Ser
 195 200 205
 Tyr Ala Ala Tyr Leu Arg Ser Ile Gly Val Asp Ala Trp Arg Phe Asp
 210 215 220
 Tyr Val Lys Gly Tyr Gly Ala Trp Val Val Lys Asp Trp Leu Asn Trp
 225 230 235 240
 Trp Gly Gly Trp Ala Val Gly Glu Tyr Trp Asp Thr Asn Val Asp Ala
 245 250 255
 Leu Leu Asn Trp Ala Tyr Ser Ser Gly Ala Lys Val Phe Asp Phe Pro
 260 265 270
 Leu Tyr Tyr Lys Met Asp Glu Ala Phe Asp Asn Lys Asn Ile Pro Ala
 275 280 285
 Leu Val Ser Ala Leu Gln Asn Gly Gln Thr Val Val Ser Arg Asp Pro
 290 295 300
 Phe Lys Ala Val Thr Phe Val Ala Asn His Asp Thr Asp Ile Ile Trp
 305 310 315 320
 Asn Lys Tyr Leu Ala Tyr Ala Phe Ile Leu Thr Tyr Glu Gly Gln Pro
 325 330 335
 Val Ile Phe Tyr Arg Asp Tyr Glu Glu Trp Leu Asn Lys Asp Arg Leu
 340 345 350
 Asn Asn Leu Ile Trp Ile His Asp His Leu Ala Gly Gly Ser Thr Ser
 355 360 365
 Ile Val Tyr Tyr Asp Ser Asp Glu Met Ile Phe Val Arg Asn Gly Tyr
 370 375 380

Gly Ser Lys Pro Gly Leu Ile Thr Tyr Ile Asn Leu Gly Ser Ser Lys
 385 390 395 400
 Val Gly Arg Trp Val Tyr Val Pro Lys Phe Ala Gly Ala Cys Ile His
 405 410 415
 Glu Tyr Thr Gly Asn Leu Gly Gly Trp Val Asp Lys Tyr Val Tyr Ser
 420 425 430
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 435 440 445
 Gln Tyr Gly Tyr Ser Val Trp Ser Tyr Cys Gly Val Gly
 450 455 460

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47

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39

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33

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38

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<400> 17
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31

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<400> 24

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<400> 26

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31

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<210> 40
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<210> 41

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<400> 41
 gaacgtctca gccatgcgtc aacgccgatg 30

<210> 42
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<400> 42
 gaacgtctca ttgtagtaga gcgggaagtc g 31

<210> 43
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<400> 43
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<210> 44
 <211> 34
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 <213> Artificial Sequence

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<400> 45
 gaaccgtctc accttcggc cttgctcgag cc 32

<210> 46
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<400> 46

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35

<210> 47

<211> 50

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30

<210> 49

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 49

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31

<210> 50

<211> 33

<212> DNA

<213> Artificial Sequence

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<400> 50

gaacgtctca cctcgacttc caccgaacg agc

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31

<210> 52

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 52

gaacggtctc aacaagatgg acgaggcctt cg

32

<210> 53

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 53

gaaccgtctc acgatataat ctggaacaag

30

<210> 54

<211> 35

<212> DNA

<213> Artificial Sequence

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<223> Primer

<400> 54

gaaccgtctc agaagcactg acatcgttta ctacg

35

<210> 55

<211> 30

<212> DNA

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<223> Primer

<400> 55

gaaccgtctc aaaggtgggt ttacgttccg

30

<210> 56

<211> 30

<212> DNA

<213> Artificial Sequence

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<223> Primer

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<400> 57
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<400> 58
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gaacgtctca cgccaggcat cgatgccgat 30

<210> 60
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<400> 60
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<210> 61
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<400> 61

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<210> 62
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<400> 62
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<210> 66
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 gcgatatgga tccctcccgc gagcaagggt atgagcggcg gctattcgat gggctacgac 180
 ccctacgatt attttgacct cggtagtagc taccagaagg gaacggtgga aacgagggtc 240
 ggctcaaagc aggagctcat aaacatgata aacaccgcc acgcctatgg catgaaggta 300

atagccgata	tagtcatcaa	ccaccgcgcc	ggcggtgacc	tggagtggaa	ccccttcgtg	360
aacgactata	cctggaccga	cttctcaaag	gtcgcgtcgg	gtaaatacac	ggccaactac	420
ctcgacttcc	accgaacga	gtcccatgcg	ggcgattccg	gaacatttgg	aggctatccc	480
gacatatgcc	acgacaagag	ctgggaccag	tactggctct	gggccagcca	ggagagctac	540
gcggcatatc	tcaggagcat	cggcatcgat	gcctggcgct	tcgactacgt	caagggctat	600
gctccctggg	tcgtcaagga	ctggctgaac	tgggtggggag	gctgggcggg	tggagagtac	660
tgggacacca	acgtcgacgc	tgttctcaac	tgggcatact	cgagcgggtc	caaggtcttt	720
gacttcgccc	tctactacaa	gatggacgag	gccttcgata	acaacaacat	tcccgccttg	780
gtggacgccc	tcagatacgg	tcagacagtg	gtcagccgcg	acccgttcaa	ggctgtgacg	840
tttgtagcca	accacgatac	cgacataatc	tggacaaga	atccagccta	cgcgttcac	900
ctcacctacg	agggccagcc	gacaatatc	taccgcgact	acgaggagtg	gctcaacaag	960
gataagctca	agaacctcat	ctggatacat	gacaacctcg	ccggagggag	cactgacatc	1020
gtttactacg	acaacgacga	gctgatattc	gtgagaaacg	gctacggaag	caagccggga	1080
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ttcgcaggct	cgtgcataca	cgagtacacc	ggcaatctcg	gcggctgggt	ggacaagtgg	1200
gtggactcaa	gcggctgggt	ctacctcgag	gctcctgccc	acgaccggc	caacggccag	1260
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<211> 432

<212> PRT

<213> Environmental

<400> 67

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			20					25					30		
Asp	Trp	Ala	Ser	Ala	Gly	Ile	Ser	Ala	Ile	Trp	Ile	Pro	Pro	Ala	Ser
		35					40					45			
Lys	Gly	Met	Ser	Gly	Gly	Tyr	Ser	Met	Gly	Tyr	Asp	Pro	Tyr	Asp	Tyr
	50					55					60				
Phe	Asp	Leu	Gly	Glu	Tyr	Tyr	Gln	Lys	Gly	Thr	Val	Glu	Thr	Arg	Phe
65					70					75					80
Gly	Ser	Lys	Gln	Glu	Leu	Ile	Asn	Met	Ile	Asn	Thr	Ala	His	Ala	Tyr
				85					90					95	
Gly	Met	Lys	Val	Ile	Ala	Asp	Ile	Val	Ile	Asn	His	Arg	Ala	Gly	Gly
			100					105					110		
Asp	Leu	Glu	Trp	Asn	Pro	Phe	Val	Asn	Asp	Tyr	Thr	Trp	Thr	Asp	Phe
		115					120					125			
Ser	Lys	Val	Ala	Ser	Gly	Lys	Tyr	Thr	Ala	Asn	Tyr	Leu	Asp	Phe	His
	130					135					140				
Pro	Asn	Glu	Leu	His	Ala	Gly	Asp	Ser	Gly	Thr	Phe	Gly	Gly	Tyr	Pro
145				150					155						160
Asp	Ile	Cys	His	Asp	Lys	Ser	Trp	Asp	Gln	Tyr	Trp	Leu	Trp	Ala	Ser
			165						170					175	
Gln	Glu	Ser	Tyr	Ala	Ala	Tyr	Leu	Arg	Ser	Ile	Gly	Ile	Asp	Ala	Trp
			180					185					190		
Arg	Phe	Asp	Tyr	Val	Lys	Gly	Tyr	Ala	Pro	Trp	Val	Val	Lys	Asp	Trp
		195					200					205			
Leu	Asn	Trp	Trp	Gly	Gly	Trp	Ala	Val	Gly	Glu	Tyr	Trp	Asp	Thr	Asn
	210					215					220				
Val	Asp	Ala	Val	Leu	Asn	Trp	Ala	Tyr	Ser	Ser	Gly	Ala	Lys	Val	Phe
225				230					235						240
Asp	Phe	Ala	Leu	Tyr	Tyr	Lys	Met	Asp	Glu	Ala	Phe	Asp	Asn	Asn	Asn
			245					250					255		
Ile	Pro	Ala	Leu	Val	Asp	Ala	Leu	Arg	Tyr	Gly	Gln	Thr	Val	Val	Ser

260	265	270
Arg Asp Pro Phe Lys Ala Val Thr	Phe Val Ala Asn His Asp Thr Asp	
275	280	285
Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe	Ile Leu Thr Tyr Glu	
290	295	300
Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu	Glu Trp Leu Asn Lys	
305	310	315
Asp Lys Leu Lys Asn Leu Ile Trp Ile His Asp	Asn Leu Ala Gly Gly	
325	330	335
Ser Thr Asp Ile Val Tyr Tyr Asp Asn Asp Glu	Leu Ile Phe Val Arg	
340	345	350
Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile Thr Tyr	Ile Asn Leu Ala	
355	360	365
Ser Ser Lys Ala Gly Arg Trp Val Tyr Val Pro	Lys Phe Ala Gly Ser	
370	375	380
Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly	Trp Val Asp Lys Trp	
385	390	395
Val Asp Ser Ser Gly Trp Val Tyr Leu Glu Ala	Pro Ala His Asp Pro	
405	410	415
Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr	Cys Gly Val Gly	
420	425	430

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<400> 69

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Ala	Ser	Gly	Lys	Tyr	Thr	Ala	Asn	Tyr	Leu	Asp	Phe	His	Pro	Asn	Glu
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Val	Lys	Cys	Cys	Asp	Glu	Gly	Thr	Phe	Gly	Gly	Phe	Pro	Asp	Ile	Ala
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Trp	Gly	Gly	Trp	Ala	Val	Gly	Glu	Tyr	Trp	Asp	Thr	Asn	Val	Asp	Ala
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Leu	Tyr	Tyr	Lys	Met	Asp	Ala	Ala	Phe	Asp	Asn	Lys	Asn	Ile	Pro	Ala
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Leu	Val	Glu	Ala	Leu	Lys	Asn	Gly	Gly	Thr	Val	Val	Ser	Arg	Asp	Pro
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Ala	Gly	Arg	Trp	Val	Tyr	Val	Pro	Lys	Phe	Ala	Gly	Ala	Cys	Ile	His
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